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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/010,942B

DATE: 09/27/2002
TIME: 13:47:23

Input Set : A:\SeqlistCorrected.txt
Output Set: N:\CRF4\09272002\J010942B.raw

3 <110> APPLICANT: Basi, Guriq
4 Saldanha, Jose
5 Yednock, Ted
7 <120> TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
8 BETA AMYLOID PEPTIDE
10 <130> FILE REFERENCE: ELN-002
12 <140> CURRENT APPLICATION NUMBER: US 10/010,942B
C--> 13 <141> CURRENT FILING DATE: 2002-12-06
15 <150> PRIOR APPLICATION NUMBER: US 60/251,892
16 <151> PRIOR FILING DATE: 2000-12-06
18 <160> NUMBER OF SEQ ID NOS: 63
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 396
24 <212> TYPE: DNA
25 <213> ORGANISM: Mus musculus
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (1)...(396)
31 <221> NAME/KEY: sig_peptide
32 <222> LOCATION: (1)...(60)

W--> 34 <400> 1 48
35 atg atg agt cct gcc cag ttc ctg ttt ctg tta gtg ctc tgg att cg 48
36 Met Met Ser Pro Ala Gln Phe Leu Phe Leu Val Leu Trp Ile Arg -5
37 -20 -15 -10 96
39 gaa acc aac ggt tat gtt gtg atg acc cag act cca ctc act ttg tcg 96
40 Glu Thr Asn Gly Tyr Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser 10
41 1 5 10 144
43 gtt acc att gga caa cca gcc tcc atc tct tgc aag tca agt cag agc 144
44 Val Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser 25
45 15 20 25 192
47 ctc tta gat agt gat gga aag aca tat ttg aat ttg ttg tta cag agg 192
48 Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg 40
49 30 35 40 240
51 cca ggc cag tct cca aag cgc cta atc tat ctg gtg tct aaa ctg gac 240
52 Pro Gly Gln Ser Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp 60
53 45 50 55 288
55 tct gga gtc cct gac agg ttc act ggc agt gga tca ggg aca gat ttt 288
56 Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe 75
57 65 70 75 336
59 aca ctg aaa atc agc aga ata gag gct gag gat ttg gga ctt tat tat 336
60 Thr Leu Lys Ile Ser Arg Ile Glu Ala Glu Asp Leu Gly Leu Tyr Tyr 90
61 80 85

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63 tgc tgg caa ggt aca cat ttt cct cggtt gtc acc aag 384
 64 Cys Trp Gln Gly Thr His Phe Pro Arg Thr Phe Gly Gly Thr Lys
 65 95 100 105 396
 67 ctg gaa atc aaa
 68 Leu Glu Ile Lys
 69 110
 72 <210> SEQ ID NO: 2
 73 <211> LENGTH: 132
 74 <212> TYPE: PRT
 75 <213> ORGANISM: Mus musculus
 77 <220> FEATURE:
 78 <221> NAME/KEY: SIGNAL
 79 <222> LOCATION: (1)...(20)
 81 <400> SEQUENCE: 2
 82 Met Met Ser Pro Ala Gln Phe Leu Phe Leu Val Leu Trp Ile Arg -5
 83 -20 -15 -10
 84 Glu Thr Asn Gly Tyr Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser 10
 85 1 5 10
 86 Val Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser 25
 87 15 20 25
 88 Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg 40
 89 30 35 40
 90 Pro Gly Gln Ser Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp 60
 91 45 50 55 60
 92 Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe 75
 93 65 70 75
 94 Thr Leu Lys Ile Ser Arg Ile Glu Ala Glu Asp Leu Gly Leu Tyr Tyr 90
 95 80 85 90
 96 Cys Trp Gln Gly Thr His Phe Pro Arg Thr Phe Gly Gly Gly Thr Lys 105
 97 95 100 105
 98 Leu Glu Ile Lys
 99 110
 102 <210> SEQ ID NO: 3
 103 <211> LENGTH: 414
 104 <212> TYPE: DNA
 105 <213> ORGANISM: Mus musculus
 107 <220> FEATURE:
 108 <221> NAME/KEY: CDS
 109 <222> LOCATION: (1)...(414)
 111 <221> NAME/KEY: sig_peptide
 112 <222> LOCATION: (1)...(57)
 W--> 114 <400> 3 48
 115 atg aac ttc ggg ctc agc ttg att ttc ctt gtc ctt gtt tta aaa ggt 48
 116 Met Asn Phe Gly Leu Ser Leu Ile Phe Leu Val Leu Val Leu Lys Gly -5
 117 -15 -10 -5
 119 gtc cag tgt gaa gtg aag ctg gtg gag tct ggg gga ggc tta gtg aag 96
 120 Val Gln Cys Glu Val Lys Leu Val Glu Ser Gly Gly Leu Val Lys 10
 121 1 5 10
 123 cct gga gcg tct ctg aaa ctc tcc tgt gca gcc tct gga ttc act ttc 144

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124	Pro	Gly	Ala	Ser	Leu	Lys	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe
125	15				20							25				
127	agt	aac	tat	ggc	atg	tct	tgg	gtt	cgc	cag	aat	tca	gac	aag	agg	ctg
128	Ser	Asn	Tyr	Gly	Met	Ser	Trp	Val	Arg	Gln	Asn	Ser	Asp	Lys	Arg	Leu
129	30				35						40				45	
131	gag	tgg	gtt	gca	tcc	att	agg	agt	ggt	ggt	aga	acc	tac	tat	tca	
132	Glu	Trp	Val	Ala	Ser	Ile	Arg	Ser	Gly	Gly	Gly	Arg	Thr	Tyr	Tyr	Ser
133	50									55				60		
135	gac	aat	gta	aag	ggc	cga	ttc	acc	atc	tcc	aga	gag	aat	gcc	aag	aac
136	Asp	Asn	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Glu	Asn	Ala	Lys	Asn
137	65							70					75			
139	acc	ctg	tac	ctg	caa	atg	agt	ctg	aag	tct	gag	gac	acg	gcc	ttg	
140	Thr	Leu	Tyr	Leu	Gln	Met	Ser	Ser	Leu	Lys	Ser	Glu	Asp	Thr	Ala	Leu
141	80					85					90					
143	tat	tat	tgt	gtc	aga	tat	gat	cac	tat	agt	ggt	agc	tcc	gac	tac	tgg
144	Tyr	Tyr	Cys	Val	Arg	Tyr	Asp	His	Tyr	Ser	Gly	Ser	Ser	Asp	Tyr	Trp
145	95					100					105					
147	ggc	cag	ggc	acc	act	gtc	aca	gtc	tcc	tca						414
148	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Thr	Val	Ser	Ser				
149	110				115											
152	<210>	SEQ	ID	NO:	4											
153	<211>	LENGTH:	138													
154	<212>	TYPE:	PRT													
155	<213>	ORGANISM:	Mus musculus													
157	<220>	FEATURE:														
158	<221>	NAME/KEY:	SIGNAL													
159	<222>	LOCATION:	(1)...(19)													
161	<400>	SEQUENCE:	4													
162	Met	Asn	Phe	Gly	Leu	Ser	Leu	Ile	Phe	Leu	Val	Leu	Val	Leu	Lys	Gly
163					-15				-10					-5		
164	Val	Gln	Cys	Glu	Val	Lys	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Lys
165					1			5			10					
166	Pro	Gly	Ala	Ser	Leu	Lys	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe
167							20					25				
168	Ser	Asn	Tyr	Gly	Met	Ser	Trp	Val	Arg	Gln	Asn	Ser	Asp	Lys	Arg	Leu
169						35			40			45				
170	Glu	Trp	Val	Ala	Ser	Ile	Arg	Ser	Gly	Gly	Gly	Arg	Thr	Tyr	Tyr	Ser
171						50			55			60				
172	Asp	Asn	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Glu	Asn	Ala	Lys	Asn
173						65		70			75					
174	Thr	Leu	Tyr	Leu	Gln	Met	Ser	Ser	Leu	Lys	Ser	Glu	Asp	Thr	Ala	Leu
175						80		85			90					
176	Tyr	Tyr	Cys	Val	Arg	Tyr	Asp	His	Tyr	Ser	Gly	Ser	Ser	Asp	Tyr	Trp
177						95		100			105					
178	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Thr	Val	Ser	Ser				
179	110				115											
182	<210>	SEQ	ID	NO:	5											
183	<211>	LENGTH:	132													
184	<212>	TYPE:	PRT													

RAW SEQUENCE LISTING

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DATE: 09/27/2002

TIME: 13:47:23

Input Set : A:\SeqlistCorrected.txt
 Output Set: N:\CRF4\09272002\J010942B.raw

185 <213> ORGANISM: Artificial Sequence
 187 <220> FEATURE:
 188 <221> NAME/KEY: SIGNAL
 189 <222> LOCATION: (1)...(20)
 191 <223> OTHER INFORMATION: humanized 3D6 light chain variable region
 193 <400> SEQUENCE: 5
 194 Met Met Ser Pro Ala Gln Phe Leu Phe Leu Val Leu Trp Ile Arg -5
 195 -20 -15 -10 -5
 196 Glu Thr Asn Gly Tyr Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro 10
 197 1 5 10
 198 Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser 25
 199 15 20 25
 200 Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Lys 40
 201 30 35 40
 202 Pro Gly Gln Ser Pro Gln Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp 60
 203 45 50 55 60
 204 Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Thr Asp Phe 75
 205 65 70 75
 206 Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr 90
 207 80 85 90
 208 Cys Trp Gln Gly Thr His Phe Pro Arg Thr Phe Gly Gln Gly Thr Lys 105
 209 95 100 105
 210 Val Glu Ile Lys
 211 110
 214 <210> SEQ ID NO: 6
 215 <211> LENGTH: 125
 216 <212> TYPE: PRT
 217 <213> ORGANISM: Homo sapiens
 219 <220> FEATURE:
 220 <221> NAME/KEY: SIGNAL
 221 <222> LOCATION: (1)...(13)
 223 <400> SEQUENCE: 6
 224 Met Gly Leu Leu Met Leu Trp Val Ser Gly Ser Ser Gly Asp Ile Val 1
 225 -10 -5 1
 226 Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly Glu Pro Ala 15
 227 5 10 15
 228 Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr 35
 229 20 25 30 35
 230 Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu 50
 231 40 45 50
 232 Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe 65
 233 55 60 65
 234 Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val 80
 235 70 75 80
 236 Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala Leu Gln Thr 95
 237 85 90 95
 238 Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 239 100 105 110
 241 <210> SEQ ID NO: 7

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Input Set : A:\SeqlistCorrected.txt
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242 <211> LENGTH: 100
 243 <212> TYPE: PRT
 244 <213> ORGANISM: Homo sapiens
 246 <400> SEQUENCE: 7
 247 Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
 248 1 5 10 15
 249 Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
 250 20 25 30
 251 Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 252 35 40 45
 253 Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
 254 50 55 60
 255 Asp Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
 256 65 70 75 80
 257 Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
 258 85 90 95
 259 Leu Gln Thr Pro
 260 100
 263 <210> SEQ ID NO: 8
 264 <211> LENGTH: 138
 265 <212> TYPE: PRT
 266 <213> ORGANISM: Artificial Sequence
 268 <220> FEATURE:
 269 <223> OTHER INFORMATION: Humanized 3D6 heavy chain variable region
 W--> 271 <221> NAME/KEY: SIGNAL
 272 <222> LOCATION: (1)...(19)
 W--> 274 <400> 8
 275 Met Asn Phe Gly Leu Ser Leu Ile Phe Leu Val Leu Val Leu Lys Gly
 276 -15 -10 -5
 277 Val Gln Cys Glu Val Gln Leu Leu Glu Ser Gly Gly Leu Val Gln
 278 1 5 10
 279 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 280 15 20 25
 281 Ser Asn Tyr Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 282 30 35 40 45
 283 Glu Trp Val Ala Ser Ile Arg Ser Gly Gly Arg Thr Tyr Tyr Ser
 284 50 55 60
 285 Asp Asn Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
 286 65 70 75
 287 Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu
 288 80 85 90
 289 Tyr Tyr Cys Val Arg Tyr Asp His Tyr Ser Gly Ser Ser Asp Tyr Trp
 290 95 100 105
 291 Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 292 110 115
 295 <210> SEQ ID NO: 9
 296 <211> LENGTH: 121
 297 <212> TYPE: PRT
 298 <213> ORGANISM: Homo sapiens

VERIFICATION SUMMARY DATE: 09/27/2002
PATENT APPLICATION: US/10/010,942B TIME: 13:47:24

Input Set : A:\SeqlistCorrected.txt
Output Set: N:\CRF4\09272002\J010942B.raw

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:34 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:114 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:3
L:271 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:274 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8
L:381 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:384 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:12
L:417 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:13
L:497 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:15